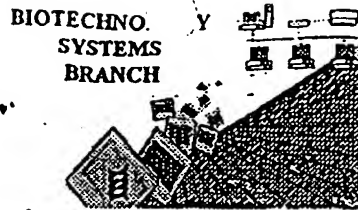


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/817,431

Source: FTO

Date Processed by STIC: 4/8/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENT IN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

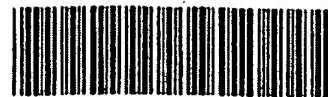
1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

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Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/8/7, 431
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/817,431

DATE: 04/08/2004
TIME: 16:14:49.

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\04082004\J817431.raw

4 <110> APPLICANT: Degussa AG
7 <120> TITLE OF INVENTION: Process for the production of L-amino acids using strains of
the
8 Enterobacteriaceae family
11 <130> FILE REFERENCE: 020489 BT
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/817,431
C--> 14 <141> CURRENT FILING DATE: 2004-04-05
14 <160> NUMBER OF SEQ ID NOS: 8
17 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 30
22 <212> TYPE: DNA
23 <213> ORGANISM: Synthetic sequence
26 <220> FEATURE:
W--> 27 <221> NAME/KEY: Primer
28 <222> LOCATION: (1)..(30)
29 <223> OTHER INFORMATION: yfid1
32 <220> FEATURE:
W--> 33 <221> NAME/KEY: Restriction site
34 <222> LOCATION: (9)..(14)
35 <223> OTHER INFORMATION: XbaI site
38 <400> SEQUENCE: 1
39 gaacaaatct agaaattaag ccggggagggc
41 <210> SEQ ID NO: 2
42 <211> LENGTH: 24
43 <212> TYPE: DNA
44 <213> ORGANISM: Synthetic sequence
47 <220> FEATURE:
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49 <222> LOCATION: (1)..(24)
50 <223> OTHER INFORMATION: yfid2
53 <220> FEATURE:
W--> 54 <221> NAME/KEY: Restriction site
55 <222> LOCATION: (8)..(13)
56 <223> OTHER INFORMATION: HindIII site
59 <400> SEQUENCE: 2
60 gctacttaag ctttacaggc tttc
62 <210> SEQ ID NO: 3
64 <211> LENGTH: 431
65 <212> TYPE: DNA
66 <213> ORGANISM: Escherichia coli
69 <220> FEATURE:
W--> 70 <221> NAME/KEY: yfid PCR product
71 <222> LOCATION: (1)..(431)

Does Not Comply
Corrected Diskette Needed

Invalid
Response

mandatory <213> Response
has to be either Art/SRI/All
Unknown or Genus/Species,
Please see item #
10 on error summary
sheet.

RAW SEQUENCE LISTING

DATE: 04/08/2004

PATENT APPLICATION: US/10/817,431

TIME: 16:14:49

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

72 <223> OTHER INFORMATION:

75 <220> FEATURE:

76 <221> NAME/KEY: CDS

77 <222> LOCATION: (36)..(419)

78 <223> OTHER INFORMATION: open reading frame yfiD

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82 gaacaaatct agaaattaag ccgaggagggc atcac atg att aca ggt atc cag 53
83 Met Ile Thr Gly Ile Gln
84 1 5
86 att act aaa gcc gct aac gac gat ctg ctg aac tct ttc tgg ctg ctg 101
87 Ile Thr Lys Ala Ala Asn Asp Asp Leu Leu Asn Ser Phe Trp Leu Leu
88 10 15 20
90 gac agc gaa aaa ggc gaa gcg cgt tgc atc gtt gca aaa gca ggt tat 149
91 Asp Ser Glu Lys Gly Glu Ala Arg Cys Ile Val Ala Lys Ala Gly Tyr
92 25 30 35
94 gca gaa gat gaa gtg gtt gca gta agc aaa ctg ggt gac att gaa tac 197
95 Ala Glu Asp Glu Val Val Ala Val Ser Lys Leu Gly Asp Ile Glu Tyr
96 40 45 50
98 cgt gaa gtt cca gta gaa gtg aaa cca gaa gtt cgc gtt gaa ggt ggt 245
99 Arg Glu Val Pro Val Glu Val Lys Pro Glu Val Arg Val Glu Gly Gly
100 55 60 65 70
102 caa cac ctg aac gtt aac gtt ctg cgt cgc gaa act ctg gaa gat gca 293
103 Gln His Leu Asn Val Asn Val Leu Arg Arg Glu Thr Leu Glu Asp Ala
104 75 80 85
106 gtt aag cat ccg gaa aaa tat ccg cag ctg acc atc cgt gta tcc ggt 341
107 Val Lys His Pro Glu Lys Tyr Pro Gln Leu Thr Ile Arg Val Ser Gly
108 90 95 100
110 tat gca gtt cgc ttt aac tct ctg act ccg gaa cag cag cgc gac gtt 389
111 Tyr Ala Val Arg Phe Asn Ser Leu Thr Pro Glu Gln Gln Arg Asp Val
112 105 110 115
114 atc gct cgt acc ttt act gaa agc ctg taa agcttaagta gc 431
115 Ile Ala Arg Thr Phe Thr Glu Ser Leu
116 120 125
119 <210> SEQ ID NO: 4
120 <211> LENGTH: 127
121 <212> TYPE: PRT
122 <213> ORGANISM: Escherichia coli
125 <400> SEQUENCE: 4
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127 1 5 10 15
129 Asn Ser Phe Trp Leu Leu Asp Ser Glu Lys Gly Glu Ala Arg Cys Ile
130 20 25 30
132 Val Ala Lys Ala Gly Tyr Ala Glu Asp Glu Val Val Ala Val Ser Lys
133 35 40 45
135 Leu Gly Asp Ile Glu Tyr Arg Glu Val Pro Val Glu Val Lys Pro Glu
136 50 55 60
138 Val Arg Val Glu Gly Gly Gln His Leu Asn Val Asn Val Leu Arg Arg
139 65 70 75 80
141 Glu Thr Leu Glu Asp Ala Val Lys His Pro Glu Lys Tyr Pro Gln Leu

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/817,431

DATE: 04/08/2004

TIME: 16:14:49

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

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142          85          90          95
144 Thr Ile Arg Val Ser Gly Tyr Ala Val Arg Phe Asn Ser Leu Thr Pro
145          100          105          110
147 Glu Gln Gln Arg Asp Val Ile Ala Arg Thr Phe Thr Glu Ser Leu
148          115          120          125
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151 <211> LENGTH: 28
152 <212> TYPE: DNA
153 <213> ORGANISM: Synthetic sequence
156 <220> FEATURE:
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158 <222> LOCATION: (1)..(28)
159 <223> OTHER INFORMATION: pflB1
162 <220> FEATURE:
W--> 163 <221> NAME/KEY: Restriction site
164 <222> LOCATION: (5)..(10)
165 <223> OTHER INFORMATION: XbaI site
168 <400> SEQUENCE: 5
169 ccactctaga aggtagggtgt tacatgtc
171 <210> SEQ ID NO: 6
172 <211> LENGTH: 27
173 <212> TYPE: DNA
174 <213> ORGANISM: Synthetic sequence
177 <220> FEATURE:
W--> 178 <221> NAME/KEY: Primer
179 <222> LOCATION: (1)..(27)
180 <223> OTHER INFORMATION: pflB2
183 <220> FEATURE:
W--> 184 <221> NAME/KEY: Restriction site
185 <222> LOCATION: (13)..(18)
186 <223> OTHER INFORMATION: HindIII site
189 <400> SEQUENCE: 6
190 cgatttcagt caaagcttat tacatag
193 <210> SEQ ID NO: 7
194 <211> LENGTH: 2325
195 <212> TYPE: DNA
196 <213> ORGANISM: Escherichia coli
199 <220> FEATURE:
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201 <222> LOCATION: (1)..(2325)
202 <223> OTHER INFORMATION:
205 <220> FEATURE:
206 <221> NAME/KEY: CDS
207 <222> LOCATION: (24)..(2306)
208 <223> OTHER INFORMATION: pflB coding region
W--> 211 <400> 7
212 ccactctaga aggtagggtgt tac atg tcc gag ctt aat gaa aag tta gcc aca
213          Met Ser Glu Leu Asn Glu Lys Leu Ala Thr
214          1          5          10

```

28

27

53

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING

DATE: 04/08/2004

PATENT APPLICATION: US/10/817,431

TIME: 16:14:49

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

216	gcc	tgg	gaa	ggt	ttt	acc	aaa	ggt	gac	tgg	cag	aat	gaa	'gta	aac	gtc	101
217	Ala	Trp	Glu	Gly	Phe	Thr	Lys	Gly	Asp	Trp	Gln	Asn	Glu	Val	Asn	Val	
218				15					20					25			
220	cgt	gac	ttc	att	cag	aaa	aac	tac	act	ccg	tac	gag	ggt	gac	gag	tcc	149
221	Arg	Asp	Phe	Ile	Gln	Lys	Asn	Tyr	Thr	Pro	Tyr	Glu	Gly	Asp	Glu	Ser	
222				30					35					40			
224	ttc	ctg	gct	ggc	gct	act	gaa	gcg	acc	acc	acc	ctg	tgg	gac	aaa	gta	197
225	Phe	Leu	Ala	Gly	Ala	Thr	Glu	Ala	Thr	Thr	Thr	Leu	Trp	Asp	Lys	Val	
226			45					50						55			
228	atg	gaa	ggc	ggt	aaa	ctg	gaa	aac	cgc	act	cac	gcg	cca	ggt	gac	ttt	245
229	Met	Glu	Gly	Val	Lys	Leu	Glu	Asn	Arg	Thr	His	Ala	Pro	Val	Asp	Phe	
230		60					65					70					
232	gac	acc	gct	ggt	gct	tcc	acc	atc	acc	tct	cac	gac	gct	ggc	tac	atc	293
233	Asp	Thr	Ala	Val	Ala	Ser	Thr	Ile	Thr	Ser	His	Asp	Ala	Gly	Tyr	Ile	
234	75				80						85				90		
236	aac	aag	cag	ctt	gag	aaa	atc	ggt	ggt	ctg	cag	act	gaa	gct	ccg	ctg	341
237	Asn	Lys	Gln	Leu	Glu	Lys	Ile	Val	Gly	Leu	Gln	Thr	Glu	Ala	Pro	Leu	
238				95					100					105			
240	aaa	cgt	gct	ctt	atc	ccg	ttc	ggt	ggt	atc	aaa	atg	atc	gaa	ggt	tcc	389
241	Lys	Arg	Ala	Leu	Ile	Pro	Phe	Gly	Gly	Ile	Lys	Met	Ile	Glu	Gly	Ser	
242				110					115					120			
244	tgc	aaa	gcg	tac	aac	cgc	gaa	ctg	gat	ccg	atg	atc	aaa	aaa	atc	ttc	437
245	Cys	Lys	Ala	Tyr	Asn	Arg	Glu	Leu	Asp	Pro	Met	Ile	Lys	Lys	Ile	Phe	
246			125					130					135				
248	act	gaa	tac	cgt	aaa	act	cac	aac	cag	ggc	gtg	ttc	gac	ggt	tac	act	485
249	Thr	Glu	Tyr	Arg	Lys	Thr	His	Asn	Gln	Gly	Val	Phe	Asp	Val	Tyr	Thr	
250		140					145					150					
252	ccg	gac	atc	ctg	cgt	tgc	cgt	aaa	tct	ggt	ggt	ctg	acc	ggt	ctg	cca	533
253	Pro	Asp	Ile	Leu	Arg	Cys	Arg	Lys	Ser	Gly	Val	Leu	Thr	Gly	Leu	Pro	
254	155				160						165				170		
256	gat	gca	tat	ggc	cgt	ggc	cgt	atc	atc	ggt	gac	tac	cgt	cgc	ggt	gcg	581
257	Asp	Ala	Tyr	Gly	Arg	Gly	Arg	Ile	Ile	Gly	Asp	Tyr	Arg	Arg	Val	Ala	
258				175						180				185			
260	ctg	tac	ggt	atc	gac	tac	ctg	atg	aaa	gac	aaa	ctg	gca	cag	ttc	act	629
261	Leu	Tyr	Gly	Ile	Asp	Tyr	Leu	Met	Lys	Asp	Lys	Leu	Ala	Gln	Phe	Thr	
262				190					195					200			
264	tct	ctg	cag	gct	gat	ctg	gaa	aac	ggc	gta	aac	ctg	gaa	cag	act	atc	677
265	Ser	Leu	Gln	Ala	Asp	Leu	Glu	Asn	Gly	Val	Asn	Leu	Glu	Gln	Thr	Ile	
266			205					210						215			
268	cgt	ctg	cgc	gaa	gaa	atc	gct	gaa	cag	cac	cgc	gct	ctg	ggt	cag	atg	725
269	Arg	Leu	Arg	Glu	Glu	Ile	Ala	Glu	Gln	His	Arg	Ala	Leu	Gly	Gln	Met	
270		220					225					230					
272	aaa	gaa	atg	gct	gcg	aaa	tac	ggc	tac	gac	atc	tct	ggt	ccg	gct	acc	773
273	Lys	Glu	Met	Ala	Ala	Lys	Tyr	Gly	Tyr	Asp	Ile	Ser	Gly	Pro	Ala	Thr	
274	235				240						245				250		
276	aac	gct	cag	gaa	gct	atc	cag	tgg	act	tac	ttc	ggc	tac	ctg	gct	gct	821
277	Asn	Ala	Gln	Glu	Ala	Ile	Gln	Trp	Thr	Tyr	Phe	Gly	Tyr	Leu	Ala	Ala	
278				255					260					265			
280	ggt	aag	tct	cag	aac	ggt	gct	gca	atg	tcc	ttc	ggt	cgt	acc	tcc	acc	869

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/817,431

DATE: 04/08/2004

TIME: 16:14:49

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

281	Val	Lys	Ser	Gln	Asn	Gly	Ala	Ala	Met	Ser	Phe	Gly	Arg	Thr	Ser	Thr	
282				270					275					280			
284	ttc	ctg	gat	gtg	tac	atc	gaa	cgt	gac	ctg	aaa	gct	ggc	aag	atc	acc	917
285	Phe	Leu	Asp	Val	Tyr	Ile	Glu	Arg	Asp	Leu	Lys	Ala	Gly	Lys	Ile	Thr	
286			285					290					295				
288	gaa	caa	gaa	gcg	cag	gaa	atg	gtt	gac	cac	ctg	gtc	atg	aaa	ctg	cgt	965
289	Glu	Gln	Glu	Ala	Gln	Glu	Met	Val	Asp	His	Leu	Val	Met	Lys	Leu	Arg	
290		300					305					310					
292	atg	gtt	cgc	ttc	ctg	cgt	act	ccg	gaa	tac	gat	gaa	ctg	ttc	tct	ggc	1013
293	Met	Val	Arg	Phe	Leu	Arg	Thr	Pro	Glu	Tyr	Asp	Glu	Leu	Phe	Ser	Gly	
294	315					320					325					330	
296	gac	ccg	atc	tgg	gca	acc	gaa	tct	atc	ggt	ggt	atg	ggc	ctc	gac	ggt	1061
297	Asp	Pro	Ile	Trp	Ala	Thr	Glu	Ser	Ile	Gly	Gly	Met	Gly	Leu	Asp	Gly	
298				335						340				345			
300	cgt	acc	ctg	gtt	acc	aaa	aac	agc	ttc	cgt	ctg	aac	acc	ctg	tac		1109
301	Arg	Thr	Leu	Val	Thr	Lys	Asn	Ser	Phe	Arg	Phe	Leu	Asn	Thr	Leu	Tyr	
302				350					355					360			
304	acc	atg	ggt	ccg	tct	ccg	gaa	ccg	aac	atg	acc	att	ctg	tgg	tct	gaa	1157
305	Thr	Met	Gly	Pro	Ser	Pro	Glu	Pro	Asn	Met	Thr	Ile	Leu	Trp	Ser	Glu	
306			365				370						375				
308	aaa	ctg	ccg	ctg	aac	ttc	aag	aaa	ttc	gcc	gct	aaa	gtg	tcc	atc	gac	1205
309	Lys	Leu	Pro	Leu	Asn	Phe	Lys	Lys	Phe	Ala	Ala	Lys	Val	Ser	Ile	Asp	
310		380				385						390					
312	acc	tct	tct	ctg	cag	tat	gag	aac	gat	gac	ctg	atg	cgt	ccg	gac	ttc	1253
313	Thr	Ser	Ser	Leu	Gln	Tyr	Glu	Asn	Asp	Asp	Leu	Met	Arg	Pro	Asp	Phe	
314	395				400					405					410		
316	aac	aac	gat	gac	tac	gct	att	gct	tgc	tgc	gta	agc	ccg	atg	atc	gtt	1301
317	Asn	Asn	Asp	Asp	Tyr	Ala	Ile	Ala	Cys	Cys	Val	Ser	Pro	Met	Ile	Val	
318				415					420					425			
320	ggt	aaa	caa	atg	cag	ttc	ttc	ggt	gcg	cgt	gca	aac	ctg	gcg	aaa	acc	1349
321	Gly	Lys	Gln	Met	Gln	Phe	Phe	Gly	Ala	Arg	Ala	Asn	Leu	Ala	Lys	Thr	
322				430					435					440			
324	atg	ctg	tac	gca	atc	aac	ggc	ggc	gtt	gac	gaa	aaa	ctg	aaa	atg	cag	1397
325	Met	Leu	Tyr	Ala	Ile	Asn	Gly	Gly	Val	Asp	Glu	Lys	Leu	Lys	Met	Gln	
326			445				450						455				
328	gtt	ggt	ccg	aag	tct	gaa	ccg	atc	aaa	ggc	gat	gtc	ctg	aac	tat	gat	1445
329	Val	Gly	Pro	Lys	Ser	Glu	Pro	Ile	Lys	Gly	Asp	Val	Leu	Asn	Tyr	Asp	
330		460				465						470					
332	gaa	gtg	atg	gag	cgc	atg	gat	cac	ttc	atg	gac	tgg	ctg	gct	aaa	cag	1493
333	Glu	Val	Met	Glu	Arg	Met	Asp	His	Phe	Met	Asp	Trp	Leu	Ala	Lys	Gln	
334	475				480						485				490		
336	tac	atc	act	gca	ctg	aac	atc	atc	cac	tac	atg	cac	gac	aag	tac	agc	1541
337	Tyr	Ile	Thr	Ala	Leu	Asn	Ile	Ile	His	Tyr	Met	His	Asp	Lys	Tyr	Ser	
338				495					500					505			
340	tac	gaa	gcc	tct	ctg	atg	gcg	ctg	cac	gac	cgt	gac	gtt	atc	cgc	acc	1589
341	Tyr	Glu	Ala	Ser	Leu	Met	Ala	Leu	His	Asp	Arg	Asp	Val	Ile	Arg	Thr	
342				510					515					520			
344	atg	gcg	tgt	ggt	atc	gct	ggt	ctg	tcc	gtt	gct	gct	gac	tcc	ctg	tct	1637
345	Met	Ala	Cys	Gly	Ile	Ala	Gly	Leu	Ser	Val	Ala	Ala	Asp	Ser	Leu	Ser	

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/817,431

DATE: 04/08/2004

TIME: 16:14:50

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:48 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:54 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:70 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:81 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:72
L:157 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:163 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:178 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:184 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:200 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:211 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:202